





PCT10

RAW SEQUENCE LISTING DATE: 05/22/2002 PATENT APPLICATION: US/10/018,290A TIME: 13:47:32

Input Set : A:\DAVI149SEQLIST.TXT

4 <110> APPLICANT: Hasse, Detlef

Output Set: N:\CRF3\05222002\J018290A.raw

```
Panaccio, Michael
             Sinistaj, Meri
     8 <120> TITLE OF INVENTION: LAWSONIA DERIVED GENE AND RELATED OMPH
            POLYPEPTIDES, PEPTIDES, AND PROTEINS AND THEIR USES
    12 <130> FILE REFERENCE: DAVI149.001APC
    14 <140> CURRENT APPLICATION NUMBER: US 10/018,290A
C > 15 <141> CURRENT FILING DATE: 2002-04-16
    17 <150> PRIOR APPLICATION NUMBER: PCT/AU00/00438
    18 <151> PRIOR FILING DATE: 2000-05-11
    20 <150> PRIOR APPLICATION NUMBER: US 60/133,986
    21 <151> PRIOR FILING DATE: 1999-05-13
    23 <160> NUMBER OF SEQ ID NOS: 13
    25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    27 <210> SEQ ID NO: 1
    28 <211> LENGTH: 186
    29 <212> TYPE: PRT
    30 <213> ORGANISM: Lawsonia intracellularis
    32 <400> SEQUENCE: 1
    33 Met Lys Val Lys Thr Leu Ser Met Ala Ile Leu Ala Cys Leu Leu Val
                         5
                                            10
    35 Ala Asn Ser Ala Phe Ser Ala Asp Phe Pro Ile Gly Val Phe Asn Ser
                    20
                                        25
     37 Gln Ser Ile Ala Met Glu Ser Glu Ala Ala Lys Ala Ala Gln Lys Lys
                                    40
     39 Leu Gln Ser Glu Phe Gly Asn Glu Lys Thr Gln Leu Glu Lys Gln Ala
     41 Lys Asp Leu Gln Thr Lys Ala Asp Asp Leu Gln Ala Lys Ser Ala Ala
     43 Met Ser Asn Gln Ala Arg Glu Asp Lys Gln Arg Glu Phe Leu Glu Leu
                                            90
    45 Arg Arg Asn Phe Glu Glu Lys Ser Arg Asp Phe Ala Ile Arg Val Glu
                                        105
     47 Gln Ala Glu Asn Thr Leu Arg Gln Tyr Leu Ala Glu Gln Ile Tyr Leu
                115
                                    120
     49 Ala Ala Glu Thr Ile Ala Lys Lys Lys Gly Leu Lys Leu Val Leu Asp
                                135
           130
                                                    140
    51 Ser Ala Ser Gly Ser Val Met Tyr Leu Glu Lys Asn Leu Asp Ile Thr
                            150
                                                155
    53 Lys Glu Ile Leu Glu Ala Ile Asn Ala Ala Trp Lys Lys Gly Gly Ser
                        165
                                            170
     55 Lys Leu Pro Glu Met Ala Asn Arg Lys Lys
                    180
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```
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 561
61 <212> TYPE: DNA
62 <213> ORGANISM: Lawsonia intracellularis
64 <220> FEATURE:
65 <221> NAME/KEY: CDS
66 <222> LOCATION: (1)...(561)
68 <400> SEQUENCE: 2
69 atg aaa gta aaa act ctt tcc atg gct att tta gct tgt tta tta gta
70 Met Lys Val Lys Thr Leu Ser Met Ala Ile Leu Ala Cys Leu Leu Val
73 gct aac agt gca ttt tcg gct gac ttc cct att ggt gtc ttt aat tct
74 Ala Asn Ser Ala Phe Ser Ala Asp Phe Pro Ile Gly Val Phe Asn Ser
75
                20
                                    25
77 caa tcc att gcc atg gag agt gaa gca gct aag gcc gct caa aaa aaa
78 Gln Ser Ile Ala Met Glu Ser Glu Ala Ala Lys Ala Ala Gln Lys Lys
81 tta caa tca gaa ttt ggt aat gaa aaa aca caa ctt gaa aaa caa gca
82 Leu Gln Ser Glu Phe Gly Asn Glu Lys Thr Gln Leu Glu Lys Gln Ala
85 aaa gat ttg caa aca aaa gct gat gat tta caa gct aag tca gca gct
86 Lys Asp Leu Gln Thr Lys Ala Asp Asp Leu Gln Ala Lys Ser Ala Ala
87 65
                        70
                                            75
89 atg tct aac caa gca cgt gaa gat aaa caa aga gaa ttt ctt gaa ctt
90 Met Ser Asn Gln Ala Arg Glu Asp Lys Gln Arg Glu Phe Leu Glu Leu
93 cgt cgt aat ttc gaa gaa aaa tct cgt gac ttt gca ata cgt gtc gaa
94 Arg Arg Asn Phe Glu Glu Lys Ser Arg Asp Phe Ala Ile Arg Val Glu
               100
                                   105
                                                       110
97 caa get gaa aac aca tta egt caa tat eta get gaa caa ate tat ett
98 Gln Ala Glu Asn Thr Leu Arg Gln Tyr Leu Ala Glu Gln Ile Tyr Leu
                               120
           115
101 gct gct gaa act ata gca aaa aag aaa ggg tta aaa ctt gtt ctt gat
102 Ala Ala Glu Thr Ile Ala Lys Lys Gly Leu Lys Leu Val Leu Asp
                                               140
                            135
105 agt get agt gga agt gta atg tac ett gaa aaa aat eta gat att aca
                                                                       480
106 Ser Ala Ser Gly Ser Val Met Tyr Leu Glu Lys Asn Leu Asp Ile Thr
107 145
                        150
                                            155
109 aaa gaa att ctt gaa gcc ata aat gct gca tgg aaa aaa ggt gga agt
                                                                       528
110 Lys Glu Ile Leu Glu Ala Ile Asn Ala Ala Trp Lys Lys Gly Gly Ser
                    165
113 aaa ctt cca gag atg gca aac cgg aaa aaa taa
                                                                       561
114 Lys Leu Pro Glu Met Ala Asn Arg Lys Lys
118 <210> SEQ ID NO: 3
119 <211> LENGTH: 23
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
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```
124 <223> OTHER INFORMATION: oligonucleotide primer RA176 forward
126 <400> SEQUENCE: 3
127 tttattcatt cagaaggagc ttc
                                                                       23
129 <210> SEQ ID NO: 4
130 <211> LENGTH: 21
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: oligonucleotide primer RA177 reverse
137 <400> SEQUENCE: 4
                                                                       21
138 aagtttagca atttctgaaa g
140 <210> SEQ ID NO: 5
141 <211> LENGTH: 143
142 <212> TYPE: PRT
143 <213> ORGANISM: Yersinia pseudotuberculosis
145 <400> SEQUENCE: 5
146 Ser Ser Ile Phe Gln Gln Leu Pro Ala Arg Glu Ala Val Ala Ala Gly
147 1
148 Lys Lys Gln Leu Glu Asn Glu Phe Lys Gly Arg Ala Thr Glu Leu Gln
                20
150 Gly Ile Ala Ile Val Asn Val Met Glu Arg Asp Leu Gln Thr Lys Met
           35
                                40
152 Gln Lys Leu Gln Arg Asp Gly Ser Thr Met Lys Ala Ser Asp Arg Thr
                            55
154 Lys Ile Leu Ser Arg Ile Gln Asp Ala Val Lys Ser Val Ala Thr Leu
156 Glu Asn Glu Val Met Lys Gln Arg Glu Thr Lys Gly Gly Tyr Asp Val
                    85
158 Val Ile Asp Ala Asn Ala Val Ala Tyr Ala Asp Ser Ser Phe Ser Thr
                                    105
160 Lys Ala Gln Ala Phe Glu Gln Asp Asn Arg Arg Gln Ala Glu Glu
          115
                                120
162 Arg Asn Lys Lys Asp Ile Thr Ala Asp Val Leu Lys Gln Val Lys
163
       130
166 <210> SEQ ID NO: 6
167 <211> LENGTH: 164
168 <212> TYPE: PRT
169 <213> ORGANISM: Yersinia enterocolitica
171 <400> SEQUENCE: 6
172 Met Lys Lys Ser Ser Ile Phe Gln Gln Leu Pro Ala Arg Glu Thr Val
174 Ala Trp Leu Cys Ala Ala Ser Leu Gly Leu Ala Leu Ala Ala Ser Ala
                20
                                    25
176 Arg Val Gln Ala Ala Lys Ile Lys Gln Leu Glu Asn Glu Phe Lys Gly
                                40
178 Arg Ala Thr Glu Leu Gln Gly Ala Ile Val Asn Val Met Glu Arg Asp
180 Leu Gln Thr Lys Met Gln Lys Leu Gln Arg Asp Gly Ser Thr Met Lys
181 65
                                            75
```

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```
182 Ala Ser Asp Arg Thr Lys Ile Leu Ser Arg Ile Gln Asp Ala Val Lys
184 Ser Val Ala Ser Leu Glu Asn Asp Val Met Lys Gln Arg Glu Thr Lys
               100
                                    105
186 Gly Gly Tyr Asp Val Val Ile Asp Ala Asn Ala Val Ala Tyr Ala Asp
           115
                                120
188 Pro Ser Phe Ser Thr Lys Ala Gln Ala Phe Glu Gln Asp Asn Arg Arg
                            135
190 Arg Gln Met Glu Glu Arg Asn Lys Lys Asp Ile Thr Ala Asp Val Leu
                      150
191 145
192 Lys Gln Val Lys
196 <210> SEQ ID NO: 7
197 <211> LENGTH: 197
198 <212> TYPE: PRT
199 <213> ORGANISM: Haemophilus influenzae
201 <400> SEQUENCE: 7
202 Met Lys Asn Ile Gly Tyr Ile Phe Gln His His Pro Asp Arg Gln Ala
204 Val Ala Ala Lys Val Thr Ala Leu Ala Leu Gly Ile Ala Leu Ala Ser
               20
                                    25
206 Gly Tyr Ala Ser Ala Glu Glu Lys Asp Lys Leu Asp Ala Glu Phe Lys
                                40
208 Pro Val Ala Glu Lys Leu Ala Ala Ser Lys Ile Ala Phe Ile Asn Ala
                            55
210 Lys Glu Val Asp Asp Lys Ile Ala Ala Ala Arg Lys Lys Val Glu Ala
212 Lys Val Ala Ala Leu Glu Lys Asp Ala Pro Arg Leu Arg Gln Ala Asp
                    85
                                        90
214 Ile Gln Lys Leu Leu Asp Ser Ile Gln Thr Ala Thr Asn Asn Leu Ala
               100
                                    105
216 Lys Arg Gln Gln Glu Ile Asn Lys Leu Gly Ala Ala Glu Asp Ala Glu
                                120
218 Leu Gln Lys Leu Met Gln Glu Ala Lys Gly Tyr Thr Tyr Val Leu Asp
       130
                            135
220 Ala Asn Ser Ile Val Phe Ala Val Glu Gly Leu Arg Lys Leu Gln Val
222 Glu Ala Gln Ser Lys Leu Ser Arg Lys Lys Ala Glu Leu Glu Lys Met
                    165
                                        170
224 Lys Asp Ile Thr Glu Glu Val Leu Lys Ser Ile Pro Ala Ser Glu Lys
225
                180
226 Ala Gln Glu Lys Lys
227
           195
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 162
232 <212> TYPE: PRT
233 <213> ORGANISM: Aquifex aeolicus
235 <400> SEQUENCE: 8
236 Met Glu Gly Asn Lys Val Ile Arg Glu Ser Lys Phe Ile Ala Lys Ala
```

237 1

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```
238 Gln Ile Met Lys Lys Phe Phe Ala Leu Met Thr Leu Ile Ala Gly Ile
                                    25
240 Ser Phe Ser Leu Asp Thr Glu Leu Arg Lys Glu Leu Glu Lys Tyr Gln
                                40
242 Lys Leu Ile Gln Glu Phe Ala Cys Val Asp Thr Lys Gln Lys Lys Leu
                            55
244 Glu Ala Leu Lys Lys Ser Leu Glu Ser Lys Ala Leu Ser Glu Lys Ala
245 65
                        70
                                            75
246 Lys Glu Lys Val Phe Asp Lys Val Ile Lys Ile Val Glu Ser Thr Ala
                                        90
248 Lys Lys Ala Lys Glu Ile Glu Gln Leu Glu Asp Glu Lys Lys Ile
                100
                                    105
250 Lys Ala Val Phe Asp Cys Asn Ser Met Leu Tyr Trp Asp Lys Lys Leu
251
                                                    125
252 Arg Lys Leu Gln Val Glu Ala Gln Ser Lys Leu Ser Arg Lys Lys Ala
        130
                            135
254 Glu Leu Glu Lys Met Ile Asp Ile Thr Asn Glu Val Leu Lys Glu Leu
255 145
                                            155
256 Asp Lys
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 161
262 <212> TYPE: PRT
263 <213> ORGANISM: Escherichia coli
265 <400> SEQUENCE: 9
266 Met Lys Lys Gly Ser Leu Phe Gln Gln Val Ala Gln Lys Thr Gly Val
268 Ser Trp Leu Leu Ala Ala Gly Leu Gly Leu Ala Leu Ala Thr Ser Ala
270 Gln Ala Ala Asp Lys Ile Asn Thr Leu Glu Asn Glu Phe Lys Gly Arg
                                40
272 Ala Ser Glu Leu Gln Arg Ala Ile Val Asn Met Met Glu Thr Asp Leu
                            55
274 Gln Ala Lys Met Lys Leu Gln Ser Met Lys Ala Gly Ser Asp Arg
                        70
276 Thr Lys Leu Val Thr Arg Ile Gln Thr Ala Val Lys Ser Val Ala Asn
                    85
                                        90
278 Leu Glu Lys Asp Val Met Ala Gln Arg Gln Thr Ser Gln Asp Ile Asp
                100
                                    105
280 Leu Val Val Asp Ala Asn Ala Val Ala Tyr Asn Ser Ser Asp Val Phe
281
            115
282 Ala Gln Lys Ala Gln Ala Phe Glu Gln Asp Arg Ala Arg Arg Ser Asn
                            135
284 Glu Glu Arg Gly Lys Lys Asp Ile Thr Ala Asp Val Leu Lys Gln Val
285 145
                        150
                                            155
286 Lys
290 <210> SEQ ID NO: 10
291 <211> LENGTH: 161
292 <212> TYPE: PRT
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293 <213> ORGANISM: Streptococcus typhi

RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/10/018,290A

DATE: 05/22/2002 TIME: 13:47:34

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 197,198

VERIFICATION SUMMARY

DATE: 05/22/2002

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:398 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:402 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13 L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:192